Supplementary Information for:

Physiological levels of polyamines favor writhe and limit twist in DNA

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Appendix 1 – Calculations of writhe density

After nucleation of a plectoneme, if all the additional twisting converts to writhe through plectonemic growth,

$$\frac{dWr}{dz} = \frac{dn}{dz} \tag{A1.1}$$

For a uniform helix, the writhe density is $\frac{Wr}{l_p}$, where l_p is the length of DNA absorbed in plectonemic phase and is related to the total length of DNA,

$$L = l_p + l_t \ , \tag{A1.2}$$

where l_t is the length of DNA in the stretched phase. If the end loop and the portion of DNA connecting the two phases are ignored, the measured extension, z, normalized with L will be

$$z = \frac{\rho_{th} l_t}{L}, \tag{A1.3}$$

where ρ_{th} is the contraction of stretched phase due to thermal fluctuations. Substituting for l_t from Eq. (A1.3) into Eq. (A1.2) gives

$$L = l_p + \frac{zL}{\rho_{th}} \ , \tag{A1.4}$$

which implies that

$$dz = -\frac{\rho_{th}}{L} dl_p. \tag{A1.5}$$

Substituting Eq. (A1.5) into Eq. (A1.1), gives

$$\frac{dn}{dz} = -\frac{L}{\rho_{th}}\frac{dWr}{dl_p} \ . \tag{A1.6}$$

However, if the helical angle and radius of the plectoneme does not change as it grows, then

$$\frac{dWr}{dl_p} = \frac{Wr}{l_p}. \tag{A1.7}$$

Subtituting Eq. (A1.7) into Eq. (A1.6) gives

$$\left|\frac{Wr}{l_p}\right| = \frac{\rho_{th}}{L}\left|\frac{dz}{dn}\right|^{-1} \ , \tag{A1.8}$$

which can be re-normalized to Eq. [1] of the main text.

Appendix 2 – Testing whether increased writhe density decreases twist density with unchanged linking number

The following describes a means to calculate the decrease in twist density due to an increase in writhe density under conditions of constant total linking number. The total linking number characterizing a DNA molecule is:

$$n = Tw + Wr \quad , \tag{A2.1}$$

where *Tw* is the total twist. Eq. (A2.1) can be rearranged to give

$$Tw = n - \left(\frac{Wr}{l_p}\right) l_p \quad . \tag{A2.2}$$

Rearranging terms in Eq. (A1.4) gives

$$l_p = \left(1 - \frac{z}{\rho_{th}}\right) L \quad , \tag{A2.3}$$

Substituting in Eq. (A2.2) for l_p from Eq. (A2.3) and for $\left(\frac{Wr}{l_p}\right)$ from Eq. (A1.8) produces

$$Tw = n - \frac{\rho_{th}}{L} \left|\frac{dz}{dn}\right|^{-1} \left(1 - \frac{z}{\rho_{th}}\right) L = n - \left|\frac{dz}{dn}\right|^{-1} (\rho_{th} - z) \quad . \tag{A2.4}$$

Eq. (A2.4) the total twist, Tw, is expressed in terms of measureable quantities. It can be normalized by the total contour length, L, or the total number of stress-free helical turns, LK_0, to determine the twist density. This value could be checked using another measureable quantity, n_{cr}, which must approximately equal Tw if all the added twist in excess of n_{cr} (the twist required to create the first writhe) is fully absorbed as writhe.

Supplementary Figure

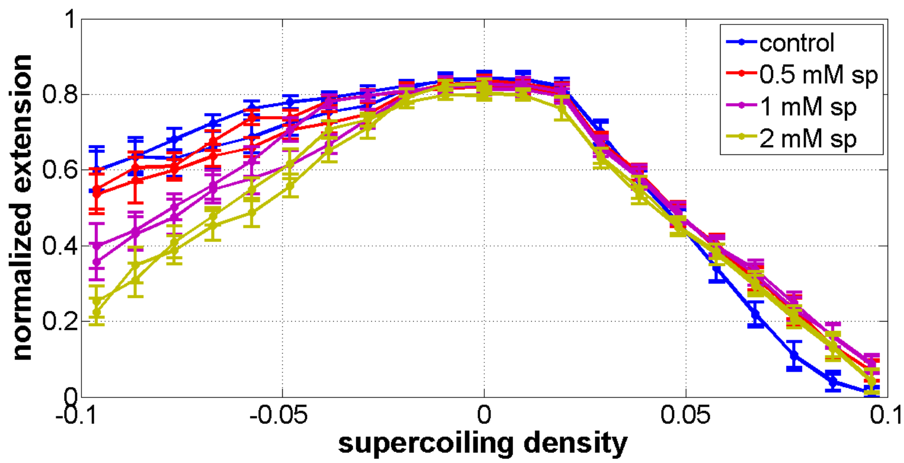

Figure S1. DNA extension vs. supercoiling density as a function of spermine concentration at 0.6 pN of tension. Addition of different concentrations of spermine, did not significantly change the standard deviations of measurements of the extension of the tether.